RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/796,868

Source: IF(WO)

Date Processed by STIC: 3/23/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS.
http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1D03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/796,868

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length
Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 ____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213> Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220>
Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa
"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

RAW SEQUENCE LISTING   DATE: 03/23/2004
PATENT APPLICATION: **US/10/796,868**   TIME: 10:57:50

Input Set : **A:\Sequence Listing 0942.285000K.ST25.txt**
Output Set: **N:\CRF4\03232004\J796868.raw**

```
         3  <110> APPLICANT: Hartley, James L.
         4         Brasch, Michael A.
         6  <120> TITLE OF INVENTION: Recombinational Cloning Using Engineered Recombination Sites
         8  <130> FILE REFERENCE: 0942.285000K
C-->    10  <140> CURRENT APPLICATION NUMBER: US/10/796,868
C-->    10  <141> CURRENT FILING DATE: 2004-03-10
        10  <150> PRIOR APPLICATION NUMBER: US 09/498,074
        11  <151> PRIOR FILING DATE: 2000-02-04
        13  <150> PRIOR APPLICATION NUMBER: US 09/005,476
        14  <151> PRIOR FILING DATE: 1998-01-12
        16  <150> PRIOR APPLICATION NUMBER: US 08/663,002
        17  <151> PRIOR FILING DATE: 1996-06-07
        19  <150> PRIOR APPLICATION NUMBER: US 08/486,139
        20  <151> PRIOR FILING DATE: 1995-06-07
        22  <160> NUMBER OF SEQ ID NOS: 35
        24  <170> SOFTWARE: PatentIn version 3.2
        26  <210> SEQ ID NO: 1
        27  <211> LENGTH: 25
        28  <212> TYPE: DNA
        29  <213> ORGANISM: Unknown
        31  <220> FEATURE:
        32  <223> OTHER INFORMATION: m-att core region
        35  <220> FEATURE:
        36  <221> NAME/KEY: misc_feature
        37  <222> LOCATION: (18)..(18)
        38  <223> OTHER INFORMATION: n is a, c, g, or t/u
        40  <400> SEQUENCE: 1
W-->    41  rkycwgcttt yktrtacnaa stsgb                                      25
        44  <210> SEQ ID NO: 2
        45  <211> LENGTH: 25
        46  <212> TYPE: DNA
        47  <213> ORGANISM: Unknown
        49  <220> FEATURE:
        50  <223> OTHER INFORMATION: m-attB core region
        53  <220> FEATURE:
        54  <221> NAME/KEY: misc_feature
        55  <222> LOCATION: (18)..(18)
        56  <223> OTHER INFORMATION: n is a, c, g, or t/u
        58  <400> SEQUENCE: 2
W-->    59  agccwgcttt yktrtacnaa ctsgb                                      25
        62  <210> SEQ ID NO: 3
        63  <211> LENGTH: 25
        64  <212> TYPE: DNA
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/796,868

DATE: 03/23/2004
TIME: 10:57:50

Input Set : **A:\Sequence Listing 0942.285000K.ST25.txt**
Output Set: **N:\CRF4\03232004\J796868.raw**

```
 65 <213> ORGANISM: Unknown
 67 <220> FEATURE:
 68 <223> OTHER INFORMATION: m-attR core region
 71 <220> FEATURE:
 72 <221> NAME/KEY: misc_feature
 73 <222> LOCATION: (18)..(18)
 74 <223> OTHER INFORMATION: n is a, c, g, or t/u
 76 <400> SEQUENCE: 3
```
W--> 77 gttcagcttt cktrtacnaa ctsgb   25
```
 80 <210> SEQ ID NO: 4
 81 <211> LENGTH: 25
 82 <212> TYPE: DNA
 83 <213> ORGANISM: Unknown
 85 <220> FEATURE:
 86 <223> OTHER INFORMATION: m-attL core region
 89 <220> FEATURE:
 90 <221> NAME/KEY: misc_feature
 91 <222> LOCATION: (18)..(18)
 92 <223> OTHER INFORMATION: n is a, c, g, or t/u
 94 <400> SEQUENCE: 4
```
W--> 95 agccwgcttt cktrtacnaa gtsgb   25
```
 98 <210> SEQ ID NO: 5
 99 <211> LENGTH: 25
100 <212> TYPE: DNA
101 <213> ORGANISM: Unknown
103 <220> FEATURE:
104 <223> OTHER INFORMATION: m-attP1 core region
107 <220> FEATURE:
108 <221> NAME/KEY: misc_feature
109 <222> LOCATION: (18)..(18)
110 <223> OTHER INFORMATION: n is a, c, g, or t/u
112 <400> SEQUENCE: 5
```
W--> 113 gttcagcttt yktrtacnaa gtsgb   25
```
116 <210> SEQ ID NO: 6
117 <211> LENGTH: 25
118 <212> TYPE: DNA
119 <213> ORGANISM: Unknown
121 <220> FEATURE:
122 <223> OTHER INFORMATION: attB1 core region
124 <400> SEQUENCE: 6
125 agcctgcttt tttgtacaaa cttgt                                             25
128 <210> SEQ ID NO: 7
129 <211> LENGTH: 25
130 <212> TYPE: DNA
131 <213> ORGANISM: Unknown
133 <220> FEATURE:
134 <223> OTHER INFORMATION: attB2 core region
136 <400> SEQUENCE: 7
137 agcctgcttt cttgtacaaa cttgt                                             25
```

RAW SEQUENCE LISTING   DATE: 03/23/2004
PATENT APPLICATION: US/10/796,868   TIME: 10:57:50

Input Set : **A:\Sequence Listing 0942.285000K.ST25.txt**
Output Set: **N:\CRF4\03232004\J796868.raw**

```
140 <210> SEQ ID NO: 8
141 <211> LENGTH: 25
142 <212> TYPE: DNA
143 <213> ORGANISM: Unknown
145 <220> FEATURE:
146 <223> OTHER INFORMATION: attB3 core region
148 <400> SEQUENCE: 8
149 acccagcttt cttgtacaaa cttgt                              25
152 <210> SEQ ID NO: 9
153 <211> LENGTH: 25
154 <212> TYPE: DNA
155 <213> ORGANISM: Unknown
157 <220> FEATURE:
158 <223> OTHER INFORMATION: attR1 core region
160 <400> SEQUENCE: 9
161 gttcagcttt tttgtacaaa cttgt                              25
164 <210> SEQ ID NO: 10
165 <211> LENGTH: 25
166 <212> TYPE: DNA
167 <213> ORGANISM: Unknown
169 <220> FEATURE:
170 <223> OTHER INFORMATION: attR2 core region
172 <400> SEQUENCE: 10
173 gttcagcttt cttgtacaaa cttgt                              25
176 <210> SEQ ID NO: 11
177 <211> LENGTH: 25
178 <212> TYPE: DNA
179 <213> ORGANISM: attR3 core region
181 <400> SEQUENCE: 11
182 gttcagcttt cttgtacaaa gttgg
185 <210> SEQ ID NO: 12
186 <211> LENGTH: 25
187 <212> TYPE: DNA
188 <213> ORGANISM: Unknown
190 <220> FEATURE:
191 <223> OTHER INFORMATION: attL1 core region
193 <400> SEQUENCE: 12
194 agcctgcttt tttgtacaaa gttgg
197 <210> SEQ ID NO: 13
198 <211> LENGTH: 25
199 <212> TYPE: DNA
200 <213> ORGANISM: Unknown
202 <220> FEATURE:
203 <223> OTHER INFORMATION: attL2 core region
205 <400> SEQUENCE: 13
206 agcctgcttt cttgtacaaa gttgg
209 <210> SEQ ID NO: 14
210 <211> LENGTH: 25
211 <212> TYPE: DNA
```

(handwritten annotations)

Invalid Response — Mandatory

<213> Response has to be Artificial Unknown OR Genus Species.

please see item #10 on error summary sheet.

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

25
25
25
25

```
212 <213> ORGANISM: Unknown
214 <220> FEATURE:
215 <223> OTHER INFORMATION: attL3 core region
217 <400> SEQUENCE: 14
218 acccagcttt cttgtacaaa gttgg                                    25
221 <210> SEQ ID NO: 15
222 <211> LENGTH: 25
223 <212> TYPE: DNA
224 <213> ORGANISM: Unknown
226 <220> FEATURE:
227 <223> OTHER INFORMATION: attP1 core region
229 <400> SEQUENCE: 15
230 gttcagcttt tttgtacaaa gttgg                                    25
233 <210> SEQ ID NO: 16
234 <211> LENGTH: 25
235 <212> TYPE: DNA
236 <213> ORGANISM: Unknown
238 <220> FEATURE:
239 <223> OTHER INFORMATION: attP2,P3 core region
241 <400> SEQUENCE: 16
242 gttcagcttt cttgtacaaa gttgg                                    25
245 <210> SEQ ID NO: 17
246 <211> LENGTH: 39
247 <212> TYPE: DNA
248 <213> ORGANISM: Unknown
250 <220> FEATURE:
251 <223> OTHER INFORMATION: PCR primer used to amplify Dpn I endonuclease from plasmid
253 <400> SEQUENCE: 17
254 ccaccacaaa cgcgtccatg gaattacact ttaatttag                     39
257 <210> SEQ ID NO: 18
258 <211> LENGTH: 39
259 <212> TYPE: DNA
260 <213> ORGANISM: Unknown
262 <220> FEATURE:
263 <223> OTHER INFORMATION: PCR primer used to amplify Dpn I endonuclease from plasmid
265 <400> SEQUENCE: 18
266 ccaccacaag tcgacgcatg ccgacagcct tccaaatgt                     39
269 <210> SEQ ID NO: 19
270 <211> LENGTH: 46
271 <212> TYPE: DNA
272 <213> ORGANISM: Unknown
274 <220> FEATURE:
275 <223> OTHER INFORMATION: rf1 top oligonucleotide
277 <400> SEQUENCE: 19
278 ggccgattac gatatcccaa cgaccgaaaa cctgtatttt cagggt            46
281 <210> SEQ ID NO: 20
282 <211> LENGTH: 30
283 <212> TYPE: DNA
284 <213> ORGANISM: Unknown
```

```
286 <220> FEATURE:
287 <223> OTHER INFORMATION: rf1 bottom oligonucleotide
289 <400> SEQUENCE: 20
290 caggttttcg gtcgttggga tatcgtaatc                              30
293 <210> SEQ ID NO: 21
294 <211> LENGTH: 47
295 <212> TYPE: DNA
296 <213> ORGANISM: Unknown
298 <220> FEATURE:
299 <223> OTHER INFORMATION: rf2 top oligonucleotide
301 <400> SEQUENCE: 21
302 ggccagatta cgatatccca acgaccgaaa acctgtattt tcagggt          47
305 <210> SEQ ID NO: 22
306 <211> LENGTH: 31
307 <212> TYPE: DNA
308 <213> ORGANISM: Unknown
310 <220> FEATURE:
311 <223> OTHER INFORMATION: rf2 bottom oligonucleotide
313 <400> SEQUENCE: 22
314 caggttttcg gtcgttggga tatcgtaatc t                            31
317 <210> SEQ ID NO: 23
318 <211> LENGTH: 48
319 <212> TYPE: DNA
320 <213> ORGANISM: Unknown
322 <220> FEATURE:
323 <223> OTHER INFORMATION: rf3 top oligonucleotide
325 <400> SEQUENCE: 23
326 ggccaagatt acgatatccc aacgaccgaa aacctgtatt ttcagggt         48
329 <210> SEQ ID NO: 24
330 <211> LENGTH: 32
331 <212> TYPE: DNA
332 <213> ORGANISM: Unknown
334 <220> FEATURE:
335 <223> OTHER INFORMATION: rf3 bottom oligonucleotide
337 <400> SEQUENCE: 24
338 caggttttcg gtcgttggga tatcgtaatc tt                           32
341 <210> SEQ ID NO: 25
342 <211> LENGTH: 15
343 <212> TYPE: DNA
344 <213> ORGANISM: Unknown
346 <220> FEATURE:
347 <223> OTHER INFORMATION: carboxy top oligonucleotide
349 <400> SEQUENCE: 25
350 accgtttacg tggac                                              15
353 <210> SEQ ID NO: 26
354 <211> LENGTH: 31
355 <212> TYPE: DNA
356 <213> ORGANISM: Unknown
358 <220> FEATURE:
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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: **US/10/796,868**

DATE: 03/23/2004
TIME: 10:57:51

Input Set : **A:\Sequence Listing 0942.285000K.ST25.txt**
Output Set: **N:\CRF4\03232004\J796868.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 18
Seq#:2; N Pos. 18
Seq#:3; N Pos. 18
Seq#:4; N Pos. 18
Seq#:5; N Pos. 18

VERIFICATION SUMMARY   DATE: 03/23/2004
PATENT APPLICATION: **US/10/796,868**   TIME: 10:57:51

Input Set : **A:\Sequence Listing 0942.285000K.ST25.txt**
Output Set: **N:\CRF4\03232004\J796868.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:41 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:59 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:77 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:95 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0